

Page 2, line 2, delete "Triticum aestivum" and substitute --Triticum aestivum --.

Page 2, line 5, delete "by claims 1 to 10", and substitute --as follows--.

Pages 4-12, delete the pages in their entirety, and substitute the pages set forth as Attachment "A".

Page 14, line 11, delete "even".

Page 15, lines 10-11, delete "for about minutes".

IN THE CLAIMS

1. (amended) A set of microsatellite markers [(based on hypervariable genome sections)] for plants of the Triticum aestivum species [, as well as of] and the [Tribe] tribe Triticeae [using the polymerase chain reaction (PCR), wherein] , each of said markers comprising a sequence tagged site (STS) , which is defined by [two specific] a pair of primers, specific to a particular microsatellite sequence, each primer having an [which] average [a] length of 20 ± 3 bases and [flank] flanking the

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particular [a] microsatellite sequence, wherein each of
said [which] microsatellite markers [are amplified to
polymorphisms (PCR products of) is formed by amplification
of the microsatellite sequence by a polymerase chain
reaction, to form markers of different length []], wherein
the primer pairs are selected from at least one of the
pairs SEQ ID NO. x and SEQ ID NO. x + 1, where x = odd
numbers from 1 through 465.

2. (twice amended) The [microsatellite markers] set
of claim 1, wherein the microsatellite sequence is a
tandem-repetitive n-fold repetition of a di-, tri-, or
tetranucleotide sequence, in which $n \geq 10$.

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3. (twice amended) The [microsatellite markers] set
of claim 1, wherein the microsatellite sequence is a
composite microsatellite sequence.

4. (twice amended) The [microsatellite markers] set of
claim 1, wherein the microsatellite sequence is an
imperfect sequence, in which individual bases are mutated.

Cancel claim 5.

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6. (twice amended) A method for the preparation of a
microsatellite marker [of claim 1 for plants of the

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Triticum aestivum] for species [as well] of the [Tribe]
tribe Triticeae, [wherein] comprising the steps of:
amplifying a microsatellite sequence, in the presence
of two specific primers flanking the sequence, with a
[hypervariable genome sections (so-called microsatellites),
with the help of the] polymerase chain reaction [(PCR), are
amplified],
separating the amplified microsatellite sequence
[subsequently separated] and [detected]
identifying the separated sequence as a particular [to
polymorphous] polymorphic fragment [fragments in the
presence of two specific primers which flank a
microsatellite sequence to the left and right of each
microsatellite locus], the two primers being chosen as SEQ
ID NO. x and SEQ ID NO. x + 1, where x = odd numbers from 1
through 465.

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7. (twice amended) The method of claim 6, wherein a
gel chosen from the group consisting of highly resolving
agarose gels, native polyacrylamide gels [or] and
denaturing polyacrylamide gels are used for the [separation
of the markers] separating step.
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